RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10 526,741

Source: PCT

Date Processed by STIC: 3-13-05

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PCT

RAW SEQUENCE LISTING   DATE: 03/13/2005
PATENT APPLICATION: US/10/526,741   TIME: 12:03:02

Input Set : A:\PTO.FY.txt
Output Set: N:\CRF4\03132005\J526741.raw

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   3 <110> APPLICANT: ABURATANI, Hiroyuki
   4        MIDORIKAWA, Yutaka
   5        NAKANO, Kiyotaka
   6        OHIZUMI, Iwao
   7        ITO, Yukio
   8        TOKITA, Susumu
  10 <120> TITLE OF INVENTION: ANTIBODY AGAINST SOLUBLE N-TERMINAL PEPTIDE OR C-TERMINAL
PEPTIDE OF GPC3
  11        PRESENT IN BLOOD
W--> 0 <130> FILE REFERENCE:
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/526,741
C--> 14 <141> CURRENT FILING DATE: 2005-03-04
  16 <150> PRIOR APPLICATION NUMBER: PCT/JP02/08999
  17 <151> PRIOR FILING DATE: 2002-09-04
  19 <160> NUMBER OF SEQ ID NOS: 24
  21 <170> SOFTWARE: PatentIn Ver. 2.1
  23 <210> SEQ ID NO: 1
  24 <211> LENGTH: 31
  25 <212> TYPE: DNA
  26 <213> ORGANISM: Artificial Sequence
  28 <220> FEATURE:
  29 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
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  36 <212> TYPE: DNA
  37 <213> ORGANISM: Artificial Sequence
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  40 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
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  52 <222> LOCATION: (109)..(1851)
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  57                                                  Met Ala Gly
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59 acc gtg cgc acc gcg tgc ttg gtg gtg gcg atg ctg ctc agc ttg gac   165
60 Thr Val Arg Thr Ala Cys Leu Val Val Ala Met Leu Leu Ser Leu Asp
61      5      '               10                  15
62 ttc ccg gga cag gcg cag ccc ccg ccg ccg ccg gac gcc acc tgt   213
63 Phe Pro Gly Gln Ala Gln Pro Pro Pro Pro Pro Asp Ala Thr Cys
64   20              25              30                  35
65 cac caa gtc cgc tcc ttc ttc cag aga ctg cag ccc gga ctc aag tgg   261
66 His Gln Val Arg Ser Phe Phe Gln Arg Leu Gln Pro Gly Leu Lys Trp
67              40              45                  50
68 gtg cca gaa act ccc gtg cca gga tca gat ttg caa gta tgt ctc cct   309
69 Val Pro Glu Thr Pro Val Pro Gly Ser Asp Leu Gln Val Cys Leu Pro
70           55              60                  65
71 aag ggc cca aca tgc tgc tca aga aag atg gaa gaa aaa tac caa cta   357
72 Lys Gly Pro Thr Cys Cys Ser Arg Lys Met Glu Glu Lys Tyr Gln Leu
73          70              75                  80
74 aca gca cga ttg aac atg gaa cag ctg ctt cag tct gca agt atg gag   405
75 Thr Ala Arg Leu Asn Met Glu Gln Leu Leu Gln Ser Ala Ser Met Glu
76      85              90                  95
77 ctc aag ttc tta att att cag aat gct gcg gtt ttc caa gag gcc ttt   453
78 Leu Lys Phe Leu Ile Ile Gln Asn Ala Ala Val Phe Gln Glu Ala Phe
79 100             105             110                 115
80 gaa att gtt gtt cgc cat gcc aag aac tac acc aat gcc atg ttc aag   501
81 Glu Ile Val Val Arg His Ala Lys Asn Tyr Thr Asn Ala Met Phe Lys
82              ·120            125                 130
83 aac aac tac cca agc ctg act cca caa gct ttt gag ttt gtg ggt gaa   549
84 Asn Asn Tyr Pro Ser Leu Thr Pro Gln Ala Phe Glu Phe Val Gly Glu
85              135             140                 145
86 ttt ttc aca gat gtg tct ctc tac atc ttg ggt tct gac atc aat gta   597
87 Phe Phe Thr Asp Val Ser Leu Tyr Ile Leu Gly Ser Asp Ile Asn Val
88          150             155             160
89 gat gac atg gtc aat gaa ttg ttt gac agc ctg ttt cca gtc atc tat   645
90 Asp Asp Met Val Asn Glu Leu Phe Asp Ser Leu Phe Pro Val Ile Tyr
91      165             170             175
92 acc cag cta atg aac cca ggc ctg cct gat tca gcc ttg gac atc aat   693
93 Thr Gln Leu Met Asn Pro Gly Leu Pro Asp Ser Ala Leu Asp Ile Asn
94 180             185             190                 195
95 gag tgc ctc cga gga gca aga cgt gac ctg aaa gta ttt ggg aat ttc   741
96 Glu Cys Leu Arg Gly Ala Arg Arg Asp Leu Lys Val Phe Gly Asn Phe
97              200             205                 210
98 ccc aag ctt att atg acc cag gtt tcc aag tca ctg caa gtc act agg   789
99 Pro Lys Leu Ile Met Thr Gln Val Ser Lys Ser Leu Gln Val Thr Arg
100             215             220                 225
101 atc ttc ctt cag gct ctg aat ctt gga att gaa gtg atc aac aca act   837
102 Ile Phe Leu Gln Ala Leu Asn Leu Gly Ile Glu Val Ile Asn Thr Thr
103             230             235               240
104 gat cac ctg aag ttc agt aag gac tgt ggc cga atg ctc acc aga atg   885
105 Asp His Leu Lys Phe Ser Lys Asp Cys Gly Arg Met Leu Thr Arg Met
106    245             250             255
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110 ggt tac tgc aat gtg gtc atg caa ggc tgt atg gca ggt gtg gtg gag   981
111 Gly Tyr Cys Asn Val Val Met Gln Gly Cys Met Ala Gly Val Val Glu
112             280             285             290
113 att gac aag tac tgg aga gaa tac att ctg tcc ctt gaa gaa ctt gtg  1029
114 Ile Asp Lys Tyr Trp Arg Glu Tyr Ile Leu Ser Leu Glu Glu Leu Val
115             295             300             305
116 aat ggc atg tac aga atc tat gac atg gag aac gta ctg ctt ggt ctc  1077
117 Asn Gly Met Tyr Arg Ile Tyr Asp Met Glu Asn Val Leu Leu Gly Leu
118             310             315             320
119 ttt tca aca atc cat gat tct atc cag tat gtc cag aag aat gca gga  1125
120 Phe Ser Thr Ile His Asp Ser Ile Gln Tyr Val Gln Lys Asn Ala Gly
121         325             330             335
122 aag ctg acc acc act att ggc aag tta tgt gcc cat tct caa caa cgc  1173
123 Lys Leu Thr Thr Thr Ile Gly Lys Leu Cys Ala His Ser Gln Gln Arg
124 340             345             350             355
125 caa tat aga tct gct tat tat cct gaa gat ctc ttt att gac aag aaa  1221
126 Gln Tyr Arg Ser Ala Tyr Tyr Pro Glu Asp Leu Phe Ile Asp Lys Lys
127             360             365             370
128 gta tta aaa gtt gct cat gta gaa cat gaa gaa acc tta tcc agc cga  1269
129 Val Leu Lys Val Ala His Val Glu His Glu Glu Thr Leu Ser Ser Arg
130         375             380             385
131 aga agg gaa cta att cag aag ttg aag tct ttc atc agc ttc tat agt  1317
132 Arg Arg Glu Leu Ile Gln Lys Leu Lys Ser Phe Ile Ser Phe Tyr Ser
133         390             395             400
134 gct ttg cct ggc tac atc tgc agc cat agc cct gtg gcg gaa aac gac  1365
135 Ala Leu Pro Gly Tyr Ile Cys Ser His Ser Pro Val Ala Glu Asn Asp
136         405             410             415
137 acc ctt tgc tgg aat gga caa gaa ctc gtg gag aga tac agc caa aag  1413
138 Thr Leu Cys Trp Asn Gly Gln Glu Leu Val Glu Arg Tyr Ser Gln Lys
139 420             425             430             435
140 gca gca agg aat gga atg aaa aac cag ttc aat ctc cat gag ctg aaa  1461
141 Ala Ala Arg Asn Gly Met Lys Asn Gln Phe Asn Leu His Glu Leu Lys
142             440             445             450
143 atg aag ggc cct gag cca gtg gtc agt caa att att gac aaa ctg aag  1509
144 Met Lys Gly Pro Glu Pro Val Val Ser Gln Ile Ile Asp Lys Leu Lys
145             455             460             465
146 cac att aac cag ctc ctg aga acc atg tct atg ccc aaa ggt aga gtt  1557
147 His Ile Asn Gln Leu Leu Arg Thr Met Ser Met Pro Lys Gly Arg Val
148             470             475             480
149 ctg gat aaa aac ctg gat gag gaa ggg ttt gaa agt gga gac tgc ggt  1605
150 Leu Asp Lys Asn Leu Asp Glu Glu Gly Phe Glu Ser Gly Asp Cys Gly
151         485             490             495
152 gat gat gaa gat gag tgc att gga ggc tct ggt gat gga atg ata aaa  1653
153 Asp Asp Glu Asp Glu Cys Ile Gly Gly Ser Gly Asp Gly Met Ile Lys
154 500             505             510             515
155 gtg aag aat cag ctc cgc ttc ctt gca gaa ctg gcc tat gat ctg gat  1701
156 Val Lys Asn Gln Leu Arg Phe Leu Ala Glu Leu Ala Tyr Asp Leu Asp
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158 gtg gat gat gcg cct gga aac agt cag cag gca act ccg aag gac aac  1749
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160                535                540                545
161 gag ata agc acc ttt cac aac ctc ggg aac gtt cat tcc ccg ctg aag  1797
162 Glu Ile Ser Thr Phe His Asn Leu Gly Asn Val His Ser Pro Leu Lys
163                550                555                560
164 ctt ctc acc agc atg gcc atc tcg gtg gtg tgc ttc ttc ttc ctg gtg  1845
165 Leu Leu Thr Ser Met Ala Ile Ser Val Val Cys Phe Phe Phe Leu Val
166      565          .          570                575
167 cac tga ctgcctggtg cccagcacat gtgctgccct acagcaccct gtggtcttcc  1901
168 His
169 580
170 tcgataaagg gaaccacttt cttatttttt tctatttttt tttttttgtt atcctgtata 1961
171 cctcctccag ccatgaagta gaggactaac catgtgttat gttttcgaaa atcaaatggt 2021
172 atcttttgga ggaagataca ttttagtggt agcatataga ttgtcctttt gcaaagaaag 2081
173 aaaaaaaacc atcaagttgt gccaaattat tctcctatgt ttggctgcta gaacatggtt 2141
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180 <212> TYPE: PRT
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188 Ala Thr Cys His Gln Val Arg Ser Phe Phe Gln Arg Leu Gln Pro Gly
189                35                40                45
190 Leu Lys Trp Val Pro Glu Thr Pro Val Pro Gly Ser Asp Leu Gln Val
191      50                55                60
192 Cys Leu Pro Lys Gly Pro Thr Cys Cys Ser Arg Lys Met Glu Glu Lys
193 65                70                75                80
194 Tyr Gln Leu Thr Ala Arg Leu Asn Met Glu Gln Leu Leu Gln Ser Ala
195                85                90                95
196 Ser Met Glu Leu Lys Phe Leu Ile Ile Gln Asn Ala Ala Val Phe Gln
197                100                105                110
198 Glu Ala Phe Glu Ile Val Val Arg His Ala Lys Asn Tyr Thr Asn Ala
199                115                120                125
200 Met Phe Lys Asn Asn Tyr Pro Ser Leu Thr Pro Gln Ala Phe Glu Phe
201      130                135                140
202 Val Gly Glu Phe Phe Thr Asp Val Ser Leu Tyr Ile Leu Gly Ser Asp
203 145                150                155                160
204 Ile Asn Val Asp Asp Met Val Asn Glu Leu Phe Asp Ser Leu Phe Pro
205                165                170                175
206 Val Ile Tyr Thr Gln Leu Met Asn Pro Gly Leu Pro Asp Ser Ala Leu
207                180                185                190
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209         195             200             205
210 Gly Asn Phe Pro Lys Leu Ile Met Thr Gln Val Ser Lys Ser Leu Gln
211     210             215             220
212 Val Thr Arg Ile Phe Leu Gln Ala Leu Asn Leu Gly Ile Glu Val Ile
213 225             230             235                 240
214 Asn Thr Thr Asp His Leu Lys Phe Ser Lys Asp Cys Gly Arg Met Leu
215             245             250             255
216 Thr Arg Met Trp Tyr Cys Ser Tyr Cys Gln Gly Leu Met Met Val Lys
217         260             265             270
218 Pro Cys Gly Gly Tyr Cys Asn Val Val Met Gln Gly Cys Met Ala Gly
219     275             280             285
220 Val Val Glu Ile Asp Lys Tyr Trp Arg Glu Tyr Ile Leu Ser Leu Glu
221     290             295             300
222 Glu Leu Val Asn Gly Met Tyr Arg Ile Tyr Asp Met Glu Asn Val Leu
223 305             310             315                 320
224 Leu Gly Leu Phe Ser Thr Ile His Asp Ser Ile Gln Tyr Val Gln Lys
225             325             330             335
226 Asn Ala Gly Lys Leu Thr Thr Thr Ile Gly Lys Leu Cys Ala His Ser
227             340             345             350
228 Gln Gln Arg Gln Tyr Arg Ser Ala Tyr Tyr Pro Glu Asp Leu Phe Ile
229         355             360             365
230 Asp Lys Lys Val Leu Lys Val Ala His Val Glu His Glu Glu Thr Leu
231     370             375             380
232 Ser Ser Arg Arg Arg Glu Leu Ile Gln Lys Leu Lys Ser Phe Ile Ser
233 385             390             395                 400
234 Phe Tyr Ser Ala Leu Pro Gly Tyr Ile Cys Ser His Ser Pro Val Ala
235             405             410             415
236 Glu Asn Asp Thr Leu Cys Trp Asn Gly Gln Glu Leu Val Glu Arg Tyr
237             420             425             430
238 Ser Gln Lys Ala Ala Arg Asn Gly Met Lys Asn Gln Phe Asn Leu His
239         435             440             445
240 Glu Leu Lys Met Lys Gly Pro Glu Pro Val Val Ser Gln Ile Ile Asp
241     450             455             460
242 Lys Leu Lys His Ile Asn Gln Leu Leu Arg Thr Met Ser Met Pro Lys
243 465             470             475                 480
244 Gly Arg Val Leu Asp Lys Asn Leu Asp Glu Glu Gly Phe Glu Ser Gly
245             485             490             495
246 Asp Cys Gly Asp Asp Glu Asp Glu Cys Ile Gly Gly Ser Gly Asp Gly
247             500             505             510
248 Met Ile Lys Val Lys Asn Gln Leu Arg Phe Leu Ala Glu Leu Ala Tyr
249     515             520             525
250 Asp Leu Asp Val Asp Asp Ala Pro Gly Asn Ser Gln Gln Ala Thr Pro
251     530             535             540
252 Lys Asp Asn Glu Ile Ser Thr Phe His Asn Leu Gly Asn Val His Ser
253 545             550             555                 560
254 Pro Leu Lys Leu Leu Thr Ser Met Ala Ile Ser Val Val Cys Phe Phe
255             565             570             575
256 Phe Leu Val His
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/13/2005
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<u>Invalid Line Length:</u>
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 10

VERIFICATION SUMMARY   DATE: 03/13/2005
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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:410 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:583 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:758 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
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